

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/536,875
Source: PCP/10
Date Processed by STIC: 6/9/05

ENTERED



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/536,875

DATE: 06/09/2005

TIME: 09:39:42

Input Set : A:\038136-5001-US Sequence Listing.txt

Output Set: N:\CRF4\06092005\J536875.raw

3 <110> APPLICANT: BRIGGS, Kristen
 4 GLANCY, Todd
 5 HEIN, Mitch B.
 6 HIATT, Andrew C.
 7 KARNOUP, Anton S.
 8 ANDERSON, W.H. Kerr
 9 PAREDDY, Dayakar
 10 PETOLINO, Joseph
 11 RUBIN-WILSON, Elizabeth
 12 TAYLOR, Doug
 13 Roberts, Jean L.
 14 The Dow Chemical Company
 15 Dow Agrosciences, LLC
 16 Epicycle Pharmaceutical, Inc.
 18 <120> TITLE OF INVENTION: Plant production of immunoglobulins with reduced fucosylation
 20 <130> FILE REFERENCE: 038136-5001-US
 C--> 22 <140> CURRENT APPLICATION NUMBER: US/10/536,875
 C--> 22 <141> CURRENT FILING DATE: 2005-05-27
 22 <150> PRIOR APPLICATION NUMBER: US 60/429,385
 23 <151> PRIOR FILING DATE: 2002-11-27
 25 <150> PRIOR APPLICATION NUMBER: PCT/US03/037905
 26 <151> PRIOR FILING DATE: 2003-11-28
 28 <160> NUMBER OF SEQ ID NOS: 85
 30 <170> SOFTWARE: PatentIn version 3.1
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 1494
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Herpes simplex virus
 37 <220> FEATURE:
 38 <221> NAME/KEY: CDS
 39 <222> LOCATION: (1)..(1494)
 41 <220> FEATURE:
 42 <221> NAME/KEY: misc_feature
 43 <223> OTHER INFORMATION: HSV Heavy Chain sequence
 46 <400> SEQUENCE: 1
 47 atg gga tgg agc tgg atc ttt ctc ttc ctc ctg tca gga gct gca ggt 48
 48 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
 49 1 5 10 15
 51 gtc cat tgc cag gtt cag ctc gtg cag tca ggt gct gag gtg aag aag 96
 52 Val His Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 53 20 25 30
 55 cct ggc tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggt tcc ttc 144
 56 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe

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57	35	40	45	
59	agc tcc tat gct atc aac tgg gtg agg caa gct cct gga caa ggg ctt			192
60	Ser Ser Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu			
61	50	55	60	
63	gag tgg atg gga ggg ctc atg cct atc ttt ggg aca aca aac tac gcg			240
64	Glu Trp Met Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala			
65	65	70	75	80
67	cag aag ttc cag gac agg ctc acg att acc gcg gac gta tcc acg agt			288
68	Gln Lys Phe Gln Asp Arg Leu Thr Ile Ala Asp Val Ser Thr Ser			
69	85	90	95	
71	aca gcc tac atg caa ctg agc ggc ctg aca tat gaa gac acg gcc atg			336
72	Thr Ala Tyr Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met			
73	100	105	110	
75	tat tac tgt gcg aga gtt gcc tac atg ctt gaa cct acc gtc act gca			384
76	Tyr Tyr Cys Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala			
77	115	120	125	
79	ggt ggt ttg gac gtc tgg ggc caa ggg acc ttg gtc acc gtc tcc tcc			432
80	Gly Gly Leu Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser			
81	130	135	140	
83	gca tcc ccg acc agc ccg aag gtc ttc ccg ctg agc ctc tgt agc acc			480
84	Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr			
85	145	150	155	160
87	cag cca gat ggg aac gtc atc gcc tgc ctg gtc cag ggc ttc ttc			528
88	Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe			
89	165	170	175	
91	cct cag gag cca ctc agt gtc acc tgg agc gaa agc gga cag ggc gtc			576
92	Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val			
93	180	185	190	
95	acc gcc agg aac ttc cca ccc agc cag gat gcc tcc gga gac ctg tac			624
96	Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr			
97	195	200	205	
99	acc acg tcc agc cag ctg acc ctt ccg gcc aca cag tgc cta gcg ggc			672
100	Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly			
101	210	215	220	
103	aag tcc gtg aca tgc cac gtg aag cac tac acg aat ccc agc cag gat			720
104	Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp			
105	225	230	235	240
107	gtg act gtg ccc tgc cca gtt ccc tca act cca cct acc cca tct ccc			768
108	Val Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro			
109	245	250	255	
111	tcg act cca cct acc cca tct ccc tca tgc cac ccc agg ctg tca			816
112	Ser Thr Pro Pro Thr Pro Ser Pro Cys Cys His Pro Arg Leu Ser			
113	260	265	270	
115	ctg cac agg cct ctc gag gac ctg ctc tta ggt tcg gaa ggc aac			864
116	Leu His Arg Pro Ala Leu Glu Asp Leu Leu Gly Ser Glu Ala Asn			
117	275	280	285	
119	ctc acg tgc aca ctc acc ggc ctg aga gat gcg tca ggt gtc acc ttc			912
120	Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe			
121	290	295	300	

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123 acc tgg acg ccc tca agt ggt aag	acc gct gtt caa	ggc cca cct gag	960
124 Thr Trp Thr Pro Ser Ser Gly Lys	Ser Ala Val Gln	Gly Pro Pro Glu	
125 305	310	315	320
127 cgt gac ctc tgt ggc tgc tac agc	gtg tcc agt gtc	ctt ccg ggc tgt	1008
128 Arg Asp Leu Cys Gly Cys Tyr Ser	Val Ser Val Leu	Pro Gly Cys	
129	325	330	335
131 gcc gag cct tgg aat cat ggg aag	acc ttc act tgc	act gct gcc tac	1056
132 Ala Glu Pro Trp Asn His Gly Lys	Thr Phe Thr Cys	Thr Ala Ala Tyr	
133	340	345	350
135 ccc gag agc aag acc ccg cta acc	gcc acc ctc tcg	aaa tcc ggc aac	1104
136 Pro Glu Ser Lys Thr Pro Leu Thr	Ala Thr Leu Ser	Lys Ser Gly Asn	
137	355	360	365
139 aca ttc cgg ccc gag gtc cac	ctg ctg ccg ccg	tcg gag gag ctg	1152
140 Thr Phe Arg Pro Glu Val His	Leu Leu Pro Pro	Ser Glu Glu Leu	
141	370	375	380
143 gcc ctg aac gag ctg gtg acg	ctg acg tgc ctg	gcf cgc ggc ttc agc	1200
144 Ala Leu Asn Glu Leu Val Thr	Leu Thr Cys Leu	Ala Arg Gly Phe Ser	
145 385	390	395	400
147 ccc aag gac gtg ctg gtt cgc	tgg ctg cag ggc	tca cag gag ctg cct	1248
148 Pro Lys Asp Val Leu Val Arg	Trp Leu Gln	Gly Ser Gln Glu Leu Pro	
149	405	410	415
151 agg gag aag tac ctg act tgg	gca tcc cgg cag	ccc agc caa ggc	1296
152 Arg Glu Lys Tyr Leu Thr Trp	Ala Ser Arg Gln	Glu Pro Ser Gln Gly	
153	420	425	430
155 acc acc acc ttc gct gtg acc	tcg ata ctg cgc	gtg gca gcc gag gac	1344
156 Thr Thr Phe Ala Val Thr Ser	Ile Leu Arg Val	Ala Ala Glu Asp	
157	435	440	445
159 tgg aag aag ggt gac acc ttc	tcc tgc atg	gtg ggc cac gag gcc ctt	1392
160 Trp Lys Lys Gly Asp Thr Phe	Ser Cys Met Val	Gly His Glu Ala Leu	
161	450	455	460
163 ccg ctg gcc ttc aca cag	aag acc atc gac	cgc ttg gcg ggt aaa ccc	1440
164 Pro Leu Ala Phe Thr Gln	Lys Thr Ile Asp	Arg Leu Ala Gly Lys Pro	
165 465	470	475	480
167 acc cat gtc aat gtg tct	gtc atg gcg	gag gtg gac ggc acc tgc	1488
168 Thr His Val Asn Val Ser Val	Val Met Ala	Glu Val Asp Gly Thr Cys	
169	485	490	495
171 tac tga			1494
172 Tyr			
176 <210> SEQ ID NO: 2			
177 <211> LENGTH: 497			
178 <212> TYPE: PRT			
179 <213> ORGANISM: Herpes simplex virus			
181 <400> SEQUENCE: 2			
183 Met Gly Trp Ser Trp Ile Phe Leu	Phe Leu Ser Gly	Ala Ala Gly	
184 1	5	10	15
187 Val His Cys Gln Val Gln Leu	Val Gln Ser Gly	Ala Glu Val Lys Lys	
188	20	25	30
191 Pro Gly Ser Ser Val Lys Val	Ser Cys Lys Ala	Ser Gly Gly Ser Phe	
192	35	40	45

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195 Ser Ser Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 196 50 55 60
 199 Glu Trp Met Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala
 200 65 70 75 80
 203 Gln Lys Phe Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser
 204 85 90 95
 207 Thr Ala Tyr Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met
 208 100 105 110
 211 Tyr Tyr Cys Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala
 212 115 120 125
 215 Gly Gly Leu Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 216 130 135 140
 219 Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr
 220 145 150 155 160
 223 Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe
 224 165 170 175
 227 Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val
 228 180 185 190
 231 Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr
 232 195 200 205
 235 Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly
 236 210 215 220
 239 Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp
 240 225 230 235 240
 243 Val Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro
 244 245 250 255
 247 Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser
 248 260 265 270
 251 Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn
 252 275 280 285
 255 Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe
 256 290 295 300
 259 Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu
 260 305 310 315 320
 263 Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys
 264 325 330 335
 267 Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr
 268 340 345 350
 271 Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn
 272 355 360 365
 275 Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu
 276 370 375 380
 279 Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser
 280 385 390 395 400
 283 Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro
 284 405 410 415
 287 Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly
 288 420 425 430
 291 Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp

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292	435	440	445	
295	Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu			
296	450	455	460	
299	Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro			
300	465	470	475	480
303	Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys			
304	485	490	495	
307	Tyr			
311	<210> SEQ ID NO: 3			
312	<211> LENGTH: 57			
313	<212> TYPE: DNA			
314	<213> ORGANISM: Artificial sequence			
316	<220> FEATURE:			
317	<223> OTHER INFORMATION: Heavy chain signal peptide			
319	<220> FEATURE:			
320	<221> NAME/KEY: CDS			
321	<222> LOCATION: (1)..(57)			
323	<400> SEQUENCE: 3			
324	atg gga tgg agc tgg atc ttt ctc ttc ctc ctg tca gga gct gca ggt			48
325	Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Ser Gly Ala Ala Gly			
326	1 5 10 15			
328	gtc cat tgc			57
329	Val His Cys			
333	<210> SEQ ID NO: 4			
334	<211> LENGTH: 19			
335	<212> TYPE: PRT			
336	<213> ORGANISM: Artificial sequence			
338	<220> FEATURE:			
339	<223> OTHER INFORMATION: Heavy chain signal peptide			
341	<400> SEQUENCE: 4			
343	Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly			
344	1 5 10 15			
347	Val His Cys			
351	<210> SEQ ID NO: 5			
352	<211> LENGTH: 1368			
353	<212> TYPE: DNA			
354	<213> ORGANISM: Artificial sequence			
356	<220> FEATURE:			
357	<223> OTHER INFORMATION: Mature heavy chain sequence			
359	<220> FEATURE:			
360	<221> NAME/KEY: CDS			
361	<222> LOCATION: (1)..(1368)			
363	<400> SEQUENCE: 5			
364	cag gtt cag ctc gtg cag tca ggt gct gag gtg aag aag cct ggc tcc			48
365	Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser			
366	1 5 10 15			
368	tcg gtg aag gtc tcc tgc aag gct tct gga ggt tcc ttc agc tcc tat			96
369	Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Ser Tyr			
370	20 25 30			

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/09/2005
PATENT APPLICATION: US/10/536,875 TIME: 09:39:43

Input Set : A:\038136-5001-US Sequence Listing.txt
Output Set: N:\CRF4\06092005\J536875.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:85; N Pos. 9895,9989,10099

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/536,875

DATE: 06/09/2005

TIME: 09:39:43

Input Set : A:\038136-5001-US Sequence Listing.txt
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L:22 M:270 C: Current Application Number differs, Replaced Current Application No

L:22 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:3589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:9840

M:341 Repeated in SeqNo=85